CLAIMS

1/ Process for identifying in a Gramineae, and more particularly in a maize, a nucleotide sequence orthologous to the sequence responsible for all or some of the apomictic development in an apomictic form, characterized in that mutations having a phenotype close or similar to that observed in an apomictic form are mapped in the genome of the Gramineae, more particularly that of a maize, to identify those which appear orthologous to genes involved in apomixis.

2/ Process according to claim 1, characterized in that meiotic mutations are mapped in the genome of the Gramineae, more particularly of a maize, to identify those which appear orthologous to genes involved in apomixis.

3/ Process according to claim 2, characterized in that the position of the various meiotic mutations in the genome of the Gramineae, more particularly of a maize, is located with the aid of molecular markers capable of locating the loci responsible for apomeiosis in the said apomictic form.

4/ Process according to claim 3, characterized in that molecular markers which are capable of locating the loci responsible for diplospory in *Tripsacum* are used.

5/ Process according to claim 4, characterized in that the said location relates to the *elongate* and afd loci.

6/ Process according to ~~any one of claims 1 to 5,~~ claim 1 characterized in that it also comprises tagging the meiotic mutations located, by a transposon.

7/ Process according to claim 6, characterized in that the tagging by a transposon is carried out at the *elongate* locus with the aid of transposable elements of the Mutator or Ac/Ds type.

8/ Process according to ~~any one of the above claims,~~ claim 1 characterized by the cloning and sequencing of the mutations located.

9/ Process according to claim 6 ~~or 7,~~ characterized in that the mutated genes are cloned, after the site of

insertion of the transposon has been marked by segregation analysis, and in that they are sequenced, if desired.

10/ Nucleotide sequences, characterized in that they are orthologous to the sequences responsible for all or some of the apomictic development in an apomictic form and the homologous sequences.

11/ Nucleotide sequence according to claim 10, characterized in that it corresponds to a mutated elongate gene.

12/ Nucleic acids containing one or more sequences as defined in claim 10 ~~or 11~~, associated with the regulatory sequences necessary for expression in a plant material.

13/ Cloning and expression vectors containing nucleic acids according to claim 12.

14/ Cell hosts containing a vector according to claim 13.

15/ Use of a sequence according to claim 10 or 11, if appropriate in conjunction with other alleles characteristic of apomictic forms, for introduction into the genome of a plant material, plant cells, plants at various stages of development and seeds, in order to impart to them an apomictic development.

16/ Plant cell of Gramineae, in particular of maize, characterized in that it contains in its genome at least the part of a sequence according to claim 10 ~~or 11~~ involved in an apomictic development.

17/ Plant of the family of Gramineae, in particular maize, characterized in that it contains in its genome at least the part of a sequence according to claim 10 or 11 involved in an apomictic development.

18/ Seed of Gramineae, in particular maize, characterized in that it contains in its genome at least part of a sequence according to claim 10 or 11 involved in an apomictic development.

19/ Process for the production of apomictic plants, characterized in that a nucleotide sequence according to claim 11 is used.

20/ Use of at least a part of a sequence according to claim 10 or 11 for identifying and isolating the orthologous sequences of loci in apomictic forms.

21/ Hybridization probes and molecular primers, characterized in that they are compiled from a sequence according to claim 10 or 11.

22/ Hybridization probes and molecular primers according to claim 18, characterized in that they are compiled from the *elongate* sequence.

23/ Process for identifying and isolating genes responsible for apomeiosis in apomictic *Tripsacum*, characterized in that at least a part of the sequence of the *elongate* locus is used.

24/ Process for the use of a mutagenesis population to confirm the relationship between a sequence isolated in *Tripsacum* according to claim 20 and expression of apomixis.